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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 16:43:49 ; Search time 2241.22 Seconds

(Without alignments)
11387.163 Million cell updates/sec

Title: US-09-851-670-1

Perfect score: 1547
Sequence: 1 gggagtcacatcagcagcagatg.....ttctacacatagcaggggca 1547

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenDbml: *
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34: em.htg_inv:*
35: em.htg_rod:*
36: em.htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1547	100.0	1547	6	AX026529	AX026529 Sequence
2	1547	100.0	1547	9	HS245709	AJ245709 Homo sapi
3	1545.4	99.9	1708	9	AF124141	AF124141 Homo sapi
4	1537	92.4	2811	9	AF135794	AF135794 Homo sapi
5	1434.4	92.7	1436	6	AX026530	AX026530 Sequence
6	1364.8	88.2	1570	6	AX056819	AX056819 Sequence
7	1364.8	88.2	1584	9	HS245709	AJ245709 Homo sapi
8	1358.8	87.8	1760	10	AF124142	AF124142 Homo sapi
9	1234.8	79.8	1548	10	RATRCPKC	D49836 Rat mscu
10	850.6	55.0	2277	5	AF039943	AF039943 Gallus ga
11	789.2	51.0	1808	5	AF317656	AF317656 Xenopus l
12	754.6	48.8	3536	14	AKTAKTA	M80675 AKT provir
13	751.4	48.6	2626	10	MUSRAC	X65687 M.musculus
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15	729	47.1	1617	10	RATRCPKA	D30040 Rat mRNA fo
16	722.4	46.7	2738	9	BC000479	BC000479 Homo sapi
17	721.2	46.6	2184	6	AB4523	AB4523 Sequence 13
18	719.2	46.5	2610	6	AB2733	AB2733 Sequence 3
19	719.2	46.5	2610	6	AB3232	AB3232 Sequence 1
20	719.2	46.5	2610	6	AR076381	AR076381 Sequence
21	719.2	46.5	2610	6	HUMRACPC	M63167 Human rac p
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23	716.4	46.3	2181	6	AB4455	AB4455 Sequence 70
24	698.4	45.1	1691	4	BTPEKB	X61036 B. laurus mr
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34	379.4	24.5	2134	3	AF072380	AF072380 Caenorhab
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36	364.6	23.6	2381	3	AF072381	AF072381 Caenorhab
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45	272.6	17.6	1438	9	AF085233	AF085233 Homo sapi

ALIGNMENTS

RESULT 1
AX026529
LOCUS AX026529 1547 bp DNA
DEFINITION Sequence 1 from Patent WO0037613.
ACCESSION AX026529
VERSION AX026529.1 GI:10187717
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1547)

AUTHORS Masure,S.L. and Richardson,A.

TITLE JOURNAL

Patient: WO 0037613-A 1 29-JUN-2000;

MASURE STEFAN LEO JOZER (BE) ; RICHARDSON ALAN (BE) ; JANSSEN PHARMACEUTICA NV (BE)

Location/Qualifiers

FEATURES

1..1547
/organism="Homo sapiens"

BASE COUNT 515 a 276 c 348 g 408 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
LOCUS HSA245709
DEFINITION Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).
ACCESSION AJ245709.1 GI:5604885
VERSION 1
KEYWORDS Akt-3; Akt3 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1547)
Maure, S., Hefner, B., Wesselink, J.J., Hofnagel, E., Mortier, E., Verhassel, P., Tuytelaars, A., Gordon, R., and Richardson, A.
Molecular cloning, expression and characterization of the human serine/threonine kinase Akt-3
Eur. J. Biochem. 265 (1), 353-360 (1999)
JOURNAL
MEDLINE 99421751
REFERENCE 2 (bases 1 to 1547)
Maure, S.L.
Direct Submission
Submitted (25-AUG-1999) Maure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse and at Ser472 necessary for activation, Phosphorylation at Thr305 and at Ser472 necessary for activation.
COMMENT
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Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AF124141
DEFINITION Homo sapiens protein kinase B gamma mRNA, complete cds.
ACCESSION AF124141
VERSION AF124141.1 GI:4757578
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1708)

AUTHORS Brodebeck, D., Cron, P. and Hemmings, B.A.
TITLE A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
JOURNAL J. Biol. Chem. 274 (14), 9133-9136 (1999)
REFERENCE 99194749
MEDLINE 2 (bases 1 to 1708)
AUTHORS Brodebeck, D., Cron, P. and Hemmings, B.A.
JOURNAL Direct Submission
Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerallee 66, Basel 4058, Switzerland
FEATURES
source location/Qualifiers
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BASE COUNT 554 a 327 c 372 g 455 t
ORIGIN

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Best Local Similarity 99.9%: Pred. No. 0;
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AF135794 2811 bp mRNA PRI 03-APR-2000
LOCUS AF135794
DEFINITION Homo sapiens AKT3 protein kinase mRNA, complete cds.

ACCESSION AF135794
 VERSION AF135794.1 GI:4574743
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 2811)
 AUTHORS Nakatani,K., Sakae,H., Thompson,D.A., Weigel,R.J. and Roth,R.A.
 TITLE Identification of a human Akt3 (protein kinase B gamma) which contains the regulatory serine phosphorylation site
 JOURNAL Biochem. Biophys. Res. Commun. 257 (3), 906-910 (1999)
 MEDLINE 99225329
 PUBMED 10208883
 REFERENCE 2 (bases 1 to 2811)
 AUTHORS Thompson,D.A., Nakatani,K. and Sakae,H.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1999) Surgery, MSLS Building, Room P228, 1201 Welch Road, Stanford, CA 94305, USA
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Q501.B4

BASE COUNT 905 a 506 c 582 g 818 t
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RESULT 5

AX026530 1436 bp DNA PAT 16-SEP-2000

LOCUS Sequence 2 from Patent WO0037613.

DEFINITION AX026530

ACCESSION AX026530.1 GI:10187718

VERSION

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1436)

AUTHORS Masure, S.L. and Richardson, A.

TITLE Human akt-3

JOURNAL Patent: WO 0037613-A 2 29-JUN-2000; MASURE STEPHAN LEO JOSEF (BE); RICHARDSON ALAN (BE); JANSSEN PHARMACEUTICA NV (BE)

FEATURES

source Location/Qualifiers

1. 1436

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/db_xref="taxon:9606"

BASE COUNT 487 a 248 c 329 g 372 t

ORIGIN

Query Match 92.7%; Score 1434.4; DB 6; Length 1436;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AX056819 1570 bp DNA PAT 17-JAN-2001

LOCUS Sequence 1 from Patent WO0077190.

DEFINITION AX056819

ACCESSION AX056819.1 GI:12309760

VERSION

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1570)

AUTHORS Guo, K., Ivashchenko, Y. and Clark, K.

Analysis of 500 Novel Complete Protein Coding Human cDNAs
Genome Res. 11 (3), 422-435 (2001)

PUBMED 11230166
2 (bases 1 to 1584)
REFERENCE

AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German C

research center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cdna sequencing consortium of the German Genome Project.

Information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA>.

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b 324 AAATGCCACTTAATGAAACAGACGACCAACCAACATTTATATCAGAGTCT 383

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Oy	601	cagaagatlaaagaacactagacatccctctttaaactcttgaaataatccctccagag	660
Db	744	CAGAGTATTAAGAACACTAGACATCCCTTTTAAATCATCTTGAATATTTCTTCACAGC	803
Oy	661	aaaaagccgtttgtgtctttgtgtgtgataatgcttaatggggcgagctgttttccattt	720
Db	804	AAAAGACCGTTTGTGTGTGTGTGATGGAATATGTAATGAGGGCGAGCTGTTTTCCATT	863
Oy	721	gtcagagagcgagtgctctcctgagagccgacagcttctctgtgtcgaatctgtctc	780
Db	864	GTCGAGAGACGGGTGTCTCTGTAGGAGACCCGACACTTTCATGATGTCGAGAAATGTCTC	923
Oy	781	tgacctgagactatcatatccgagaaagatgtgtatccgtgatctcctaagtgtgagaatc	840
Db	924	TGCTTGAGACTATCTACATTCGCGAAAGATGTGTCACGTCGATCTCAAGTTGAGAACT	983
Oy	841	aatgctggaagaagatgagccacaataaaatttaagaattttggaacttgaagaagaagat	900
Db	984	AATCTGTGACAAAGATGCGCACATTAATAAATTAAGATTTTGGACTTTGGAAAAGAGGAT	1043
Oy	901	cacagatgacgagccacatgtagagacatctgtgtgcaatccagaaatctgtgcacagagtc	960
Db	1044	CACAGATGCGACCACTATGAAGACATTTGTGSCACTCCAGATATMTGTGCACGAGAGT	1103
Oy	961	gttagaagataatgactatgagccgagcagtagacgtgtgtggcctagggtgtgtcaatga	1020
Db	1104	GTTTGAAGATTAATACATATGCGCAGACAGTAGACTGTGGGCGCTAAGGGGTGTATGTA	1163
Oy	1021	tgaaatgattgtgtggagaggttacctcttctacaacggagacatgagaacttttgaatt	1080
Db	1164	TGAATATATGtGtGGAGGTTTACCTTTCTACAAACCGAGACATGAGAACTTTTGAATT	1222
Oy	1081	ataataaattggaagacatlaaatttccctcgaaacactctcttaagaatgcaaaatcaatgc	1140
Db	1224	AATATTAATGGAAGACATTAATTTCTCTGCAACACTCTCTCAGATGCAAAATCATTTGCT	1283
Oy	1141	ttcagagctcttgaataaaggatcccaataaaagcctctgtgtgagaagccagatgtagcaaa	1200
Db	1284	TTTCAGGGCTCTTGATTAAGATATCAAAATAAACCCCTTGTGTGAGGACCGAGATGATGAAA	1343
Oy	1201	agaaattatgagaaacagttctctctcgtgagtaaaactgtgcagatgtagtatagtataaaa	1260
Db	1344	AGAAATTAATGAGACACAGTTTCTTCTCTGTGAGTAACCTGCAAGATGTTATGATTAATAA	1403
Oy	1261	gcttgtagctctctttaaaccctcaaglaaacatcttgagacagatactagatatltgtatga	1320
Db	1404	GCTTGATCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATTAATTTTGATGA	1463
Oy	1371	agaatttagacacttcaaatcttttgcataaagacacacttgaagaaatattga	138

DB 1464 AGAATTTCAGCTCAGACTATTACATAATAACACCTGTAATAATGTCA 1511

RESULT 8
AY005799 1695 bp mRNA PRI 01-AUG-2001
LOCUS Homo sapiens protein kinase B gamma 1 (AKT3) mRNA, complete cds.
DEFINITION alternatively spliced.
AY005799
VERSION AY005799.1 GI:15072339
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1695)
AUTHORS Brodbeck, D., Hill, M.M. and Hemmings, B.A.
TITLE Two Splice Variants of Protein Kinase B gamma Have Different
Regulatory Capacity Depending on the Presence or Absence of the
Regulatory Phosphorylation Site Serine 472 in the Carboxyl-terminal
Hydrophobic Domain
J. Biol. Chem. 276 (31), 29550-29558 (2001)
JOURNAL 11387345
PUBMED 2 (bases 1 to 1695)
REFERENCE Brodbeck, D., Cron, P., Scham, B. and Hemmings, B.A.
AUTHORS Direct Submission
TITLE Submitted (26-JUL-2000) Biochemistry, Friedrich Miescher-Institute,
JOURNAL P. O. Box 2543, Basel 4002, Switzerland
FEATURES
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1. 1695
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1. 1695
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74..1471
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lacking the Ser472 phosphorylation site; alternatively
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KVLIVREKASGRKYAMKILKEVILIAKDEVAHNTLESRLNRPFLSLKSEFOR
DLRCFMEVYNGELFFHLISREYSEDRPFGAELIVSALDYLSKGIYRDLKLEN
LMIDKDHITKTDRGLCKEGTDAATMKTTCGTPREYLAPELVLENDYGRANDMGLY
VMYEMKGRDLPFYQDHEKLFELILMEDIKRPRLSSDAKLSGLIKDNNKRLGG
PDDAKETMRHSFESGVNMQDYDKKLVPPEKPYQVTSDFRYDEFTTAQTITTPPE
KCOQSDSGMLGNMK"

BASE COUNT 572 a 315 c 383 g 425 t
ORIGIN

Query Match 88.2%; Score 1364.8; DB 9; Length 1695;
Best Local Similarity 98.4%; Pred. No. 4.3e-304;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 gggagtcacgtgagcgtgttacatgtgaaagaaggttggttcgaagaaggagga 60
DB 64 GGGAGTCATCATGACGCGATGTTACCATTTGTAAGAAAGGTGGGTTGCAAGAGGGGAGA 123

QY 61 atataaaactgagagcaagaactctcttctgaagacagatggctcatcatag 120
DB 124 ATATATAAAAGTGAAGCCAGATGATCTTCTTTGAAGACAGATGGCTCATTTATAGG 183

QY 121 atataaagaagaacctcaagatgtagattacattccctcaacaactttcagtg 180
DB 184 ATATAAGAGAAACCTCAAGATGTGATTACCTTATCCCTCAACAACCTTTTCAGTGGC 243

QY 161 aaatgccaagttaatgaaacaagaacgcacaaagccaaacacattataatcagatgctc 240
DB 244 AAAATGCCAGTTAATGAATAAGAAAGACGACCAAAAGCAACATTTATTAATCAGATGTC 303

QY 241 ccagtggactactgtctatagagaacattcatgtagatctccagaggaagaagga 300
DB 304 CCAAGTGAGACTACTGTTATAGAGAGAACATTTTCATGATACATCTCCAGAGGAAGGA 363

QY 301 atggaacaagaactaccagctgtagcagacagactgcaagggcaagaagaagaagaat 360
DB 364 ATGACAGAGAGCTATCCAGGCGTGTAGCAGACAGATCGCAGAGCAAGAAAGAGAGAA 423

QY 361 gaattgtgtccaacttcaacaataatgataataagaagaagaagaatgtagtctctac 420
DB 424 GAATTTGATGTCACACTTACAAATTTGAATAATATAGAGAGAAAGATGATGCTCTAC 483

QY 421 aaccatcataaaagaagaacatgatatgatttgactattgaaactactagtaag 480
DB 484 AACCATCATATAAAAGACACATGATGATTTTACTATTGAAACTACTAGTAAAGG 543

QY 481 caacttgggaagttatttggltcgagaagaagcaagtggaataactactatgata 540
DB 544 CACTTTGGGAAGTTATTTGGTTCGAGAGAGCAAGTGGAATAATCTATGCTATGAA 603

QY 541 gattctgagaagaagaagtcattatgcaagaagatgaatgtagcacactctcaactgaag 600
DB 604 GATTTGTGAAGAAAGATGATTTATTCAGAGAGATGATGACACACTCTTAACGAAAG 663

QY 601 cagagtatataagaacactagacatcccttcttaacatcccttgaaataatctctccagac 660
DB 664 CAGATATTATAAGAACACTAGACATCCCTTTTAAATCTCTTGAATATTTCTCTTCAGAC 723

QY 661 aaaagaccgttgglttggtagatgaatgaatgaatgaatgaatgaatgaatgaatgaat 720
DB 724 AAAAGACGTTGTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 783

QY 721 gtcgagaagaagcgggtgtctctcgagagaccgacaaagttctatgtagcaaatgtctc 780
DB 784 GTCGAGAGACCGGGTCTCTGAGAGACCGCACAGTTTCATGATGATGATGATGATGATGAT 843

QY 781 tgccttggaactatcacatcccggaagaatgtgtacgctgataccagcttgagaatct 840
DB 844 TGCCCTTGACATATCATCTACATTCGCGAAGATTTGTATGCTATCTCAAGTTGGAGATCT 903

QY 841 aatgctggaacaagaatggccaacataaaataacagatttggacttggcaagaaggat 900
DB 904 AATGCTGGAACAAAGATGCCACATTAATAATTAACAGATTTTGACTTTCAGAAAGAGGAT 963

QY 901 caccagatcagccacacatgaagaacttctgtggaactccagaatatctggaacagaagt 960
DB 964 CACAGATCCAGCCACCATGAAGACATTTGTGGCACTCCCAAAATATCTGGACCAAGAGAT 1023

QY 961 gtiagaagaatgactctgcccgaagtagactggtggggccctagaaggtgtgcatgta 1020
DB 1024 GTTACGAATATATGACTATGCGCCGAGAGTACGTGAGGGCCCTAGGGGTTGTCATGTA 1083

QY 1021 tgaatgtagtgggaaggttaacttcttacaacacaggaacatggaacttttgaatt 1080
DB 1084 TGAATGTAGTGTGGAGAGGTTAACCTTCTACAAACAGACATGAGAAACTTTTGAAT 1143

QY 1081 aatattatggaagacatlaaatttccctcgaaacactctccagatgtaaatattgct 1140
DB 1144 AATATTATATGAGACATTAATTAATTTCTCGAAGACATCTCTTTCAGATGCAAAATATCT 1203

QY 1141 ttcaaggtcttgaataaagatccaaataaagcccttggtagaagaacagatgtagcaaa 1200
DB 1204 TTCAGGCTCTTGATTAAGATGCCAATAAAGCCTTGTTGTGAGAGACAGATGATGATA 1263

QY 1201 agaaattatggaacagttctctctctgtggaataacttggcaagatgataatgataaa 1260
DB 1264 AGAATTTATGAGACACATGTTCTCTCTGAGGATTAACATGCAAGATGTATATGATTA 1323

QY 1261 gcttgactcctctttaaaccctcaagtaacatctgagacagatagatatatttgatga 1320
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Db 1324 GCTTGTAACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTGTGATGA 1383
QY 1321 agatttacagctcagactcttacaatacacacctgaaaataatgatagatgagat 1380
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Db 1384 AGAATTACAGCTCAGACTTATTAACAAACACCACTGAAAATGTGCAGAAATCAATTCAGATTG 1443
QY 1381 ggaatgcatgagacatgaga 1400
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Db 1444 TGGCATGCTGTGGTAACCTGGA 1463

RESULT 9
AF124142 1760 bp mRNA ROD 07-MAY-1999
LOCUS Mus musculus protein kinase B gamma mRNA, complete cds.
DEFINITION AF124142
ACCESSION AF124142.1 GI:4757580
VERSION
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1760)
Brodebeck, D., Cron, P. and Hemmings, B.A.
A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
J. Biol. Chem. 274 (14), 9133-9136 (1999)
JOURNAL 99194749
MEDLINE 2 (bases 1 to 1760)
Brodebeck, D., Cron, P. and Hemmings, B.A.
AUTHORS Direct Submission
TITLE Submitted (27-JAN-1999) Friedrich Miescher-Institut,
JOURNAL Maubertstrasse 66, Basel 4058, Switzerland
FEATURES
Source location/Qualifiers
1..1760
/organism="Mus musculus"
/db_xref="taxon:10090"
37..1476
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/codon_start=1
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/db_xref="GI:4757581"
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VDLPELNFSSVAKCOLMKTERPKNTPLIRLOLTVIERFHPDPEEEMTEAI
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KVIIVREKASGRTYAMKILUKREVIIAKDEVATLTESVNLKTRHPFLTSLKYSFQTK
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LMLDGHKIKITDFGLCKEGLTDAATMTFCGPPEYLAPEVLEDDYGRAVDMMLGV
VMEWMCGRLEPYNODHEKLFELILMEIDIKPFRITSSAKSLISLLIKDPKRLGGG
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KYDDGCMGMDNERPHFPFSYSASGE"

BASE COUNT 546 a 352 c 402 g 460 t
ORIGIN

Query Match 87.8%; Score 1358.8; DB 10; Length 1760;
Best Local Similarity 93.2%; Pred. No. 1e-302; Indels 4; Gaps 2;
Matches 1444; Conservative 0; Mismatches 102;

QY 1 999agtcacatcatgagcagatgttaccatgtgaaagaagcttggttcagaagaagagaga 60
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Db 27 GGGAGGCATCATGAGCGATGTTACCTGTGAAGAAGTGTGGCTTCACAAGAAGGGAGA 86
QY 61 atatatataaaacctggaggccaagatactcctttgaaagacagatggtcatlcatag 120
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Db 87 ATATATATAAAACTGGAGGCCAAGATVACTCTTTTGAAGACAGATGCTCATTCATAG 146
QY 121 atataaagagaacctcagaatgttgatttacccttaccctccacaacttttcagtgac 180
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Db 147 CTATTAAGGAAACCTCAAGATGTGACTTACCTTATCCCTCAACAACTTCTCACTGAC 206

QY 181 aaaatgcagtttaataaacaagaacagaccagaacccaacacattataatcagatgtct 240
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Db 207 AAAATCTCAAGTTAATGAAAACACAGACAGACCAAAACCAATTAATATTATATCATGATGTCT 266
QY 241 ccagttgactactgttataagagaacatttcatgtagatcctcagaagaaaggaaga 300
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Db 267 TCAGTGGACCACTGTTATAGAGAAACATTTTCATGTAGATACACAGAGAAAGAGAGAA 326
QY 301 atgacagaagaagctatccagctgttagcaacagacgagcagaggaagaagagagaa 360
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Db 327 GTGAGAGGAAGCTATCCAAAGCCGTAGCCAGCATTTGCAGAGCAAGAGAGAGAGAGAT 386
QY 361 gaattgtaccacttcaactcaaatatataataaagagaagaagatgtatgtccttac 420
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Db 387 GATTTTACGCCCAACTCCACAGATTGATATATAGAGAGAAAGAGATGATGCCCTCTAC 446
QY 421 aaccacatcaaaagaagaacaaatgaaatgtatcttgaacttgaactcagtagtaag 480
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Db 447 AACCCATCATAAAGAAAGACGATGAATGATTTTGACTATTGAACTACTAGGTAAGG 506
QY 481 cacttttggaagaatatttggtttcgaagaagaagcgaatgtgaaatctatgtctatga 540
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Db 507 CACTTTTGGGAAAGTTATTTTGGTTGAGAGAGAGCAAGCTGGAATTAATCTATGTATGAA 566
QY 541 gatttcgaagaagaagtcattatgtcgaagaatgaaatgagcagacacttaactgaag 600
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Db 567 GATTTCGAAGAAAGAAAGTATTTTTCGAAGATGAGTGAAGTCACTTTACTGTAAGG 626
QY 601 cagaatataaagaacactacagacatcccttctaactccttgaatcttccacagac 660
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Db 627 CAGAGTACTTAAGAAACACACAGACATCATTTTAAACATCTTGAATATTTCTTCAGAC 686
QY 661 aaaaagccgttggttgtgtatgaaatgtttaaagtgagggcagagcttttccattc 720
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Db 687 AAAAGACCTTTGCTGTTTGTGATGGAATATGTAATGGCGAGACCTGTTTTCATTT 746
QY 721 gtccgaagaagcggtgtctctcgaagaagcgaagcttctctatgtgtcgaagaatgtctc 780
|||||
Db 747 GTGAGAGAGAGAGTCTTCTGTGAGAGACCGCACACGCTTCTATGTGCGAATTTGTCTC 806
QY 781 tgccttgagacatcattacatcgcgaaagaatgtgtacgcgtgactcctaagtctgagaatct 840
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Db 807 TCTTTTGACATCTTCAATCTTGTGAAGAAAGATGTGTACCTGATCTCAAGTTGGAGAAATT 866
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Db 867 GATGCTAGATTAAGATGGCCATATTAATAATTCGATTTTGGCTTTCGAAAAGAGGAT 926
QY 901 caagaatgagccacacatgaagaacatctgtgtgcaactcagaatactctgacccagaagct 960
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Db 927 CACAGATGACGCTACCATTAACATCTCTGTGCGACACAGAGTACCTGACACAGAGAT 986
QY 961 gttagaagaataatgacatcagcagagcagtagacgtgtgtgagggcctaggggtgtgcatgta 1020
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Db 1047 TGAATGATGTGTGAGAGGTGCTCTTTCATCAACACAGATCATGAGAAATCTTTGGAATT 1106
QY 1081 aatatataatgagaacatataaattccctgaaacactctctcagaatgcaaaatctatgtc 1140
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Db 1107 AATACTAATGGAAGACATTAATTTCCCGGAACACTCTCTTATGATGCAAAATTCATTGCT 1166
QY 1141 ttcagggctctgtataaagaatccaaataaacyccttgggtgaggaaccagatgtatgcaaa 1200
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Db 1167 TTCAGGGGCTTGTATTAAGATTCCAAATTAAGCCCTTGTGTGAGAGGCCATGATGACAA 1226
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Db 1227 AGAAATCATGAGGACATAGTTTCTTCTGTGAGTAAATGCGCAAGATGTATATGACAAAA 1286

QY 1261 gcttgacctctttaaaccctcaagtaacatctgagacagatgactatgattgata 1320
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 QY 1321 agaattacagctcagactatatacaatacaccacctgaaataatgataagatglat 1380
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 Db 1347 ACAATTACAGCTCAGACTATTAACAATAACACACCTGAAAGTATGACAGACGGCAT 1406
 QY 1381 gacatgcataatgagagagagcgccgacattccctcaatttccctactcgaagtg 1440
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 Db 1407 GGACGCGATGACAGACGAGCGGCGACACTTCCCTCAGTTCTCTACTCTGCAAGCGG 1466
 QY 1441 acgaaataaagctcttcaatctgactcactcactcactcactcactcactcactc 1500
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 Db 1467 ACGGGAATTAAGTCTCTTCTAGCTGTCTTCTACACTGTCTCTTACTTACTTACTT 1525
 QY 1501 tgattcttgagacatc---accagctcagctcttacaacatgacagagga 1547
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 Db 1526 TGATTCTGAGCATCTCTACAGTCTGCTCTTACAGTTAGCAGAGGGA 1575

RESULT 10
 RATTRACPKG 1548 bp mRNA ROD 10-FEB-1999
 LOCUS Rat mRNA for RAC protein kinase gamma, complete cds.
 DEFINITION D49836.1 GI:1136777
 ACCESSION RAC-PK gamma; RAC protein kinase gamma.
 VERSION Rattus norvegicus brain cDNA to mRNA.
 KEYWORDS Rattus norvegicus
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 ORGANISM Rattus
 1 (bases 1 to 1548)
 Konishi, H.
 Direct Submission
 Submitted (23-MAR-1995) to the DDBJ/EMBL/GenBank databases. Hiroaki
 Konishi, Kobe University, Biosignal Research Center, Nada-ku
 Rokkoudai-cho 1-1, Kobe, Hyogo 657, Japan
 (E-mail:hkonishi@imr.kobe-u.ac.jp, Tel:078-803-1255,
 Fax:078-803-0994)
 2 (bases 1 to 1548)
 Kameyama, K., Haga, T., Tanaka, M., Matsuzaki, H., Ono, Y.,
 Konishi, H., Kuroda, S., and Kikkawa, U.
 Molecular cloning and characterization of a new member of the RAC
 protein kinase family: association of the pleckstrin homology
 domain of three types of RAC protein kinase with protein kinase C
 subtypes and beta gamma subunits of G proteins
 Biochem. Biophys. Res. Commun. 216 (2), 526-534 (1995)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 CDS
 Location/Qualifiers
 1..1548
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /tissue_type="brain"
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 /protein_id="BA06637.1"
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 KVILLREKASGRYYAMKILKREVIADDEVAHTLESVLANTHPFLTSLKYSFQK
 DRICFVMEYVNGELFFHLISREVFSEDRTEFYGAELYSADYLSHSGKTVYRDKLEN
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 KCPL"

BASE COUNT 507 a 276 c 350 g 415 t
 ORIGIN

Query Match 79.8%; Score 1234.8; DB 10; Length 1548;
 Best Local Similarity 94.0%; Pred. No. 3.8e-274;
 Matches 1284; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 QY 1 ggaagatcacaagacagatggttacatctgtgaaagaaggttggtcgaagagggaga 60
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 Db 37 GGGAGCCATCATGACGAGATGTTACATGTTAAAGACAGCTGGTTGAGAGGGAGGA 96
 QY 61 atataaaacacagagagcagaatctccttcttgaagacagatggtcactaagg 120
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 Db 97 ATATATATAAATAATGGAGGCCAAGATACCTCTTGTGAAGACAGCGGCTCATTCATAGG 156
 QY 121 atataaagaacacacacagatggtgattactatccctcacaacttctgagtc 180
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 Db 157 CTATTAAGAGAACTCAGAGATGTGACTTACTTATCCCTCAACAACTTCTCAGTGGC 216
 QY 181 aaaaagcagttatgaaacagaaacagaaacacaaacacattatcatatgct 240
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 Db 217 AAAATGTCAATTAATGAAGAAACAGAACGACCAAGCCAAATACATTTATTCAGATGCT 276
 QY 241 ccagtgagactctgttataagagagacatttcaatgatactccagaggaaggaaga 300
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 Db 277 TCAGTGGACCACTGTTATAGAGAAACATTCATGTAGTACTCCAGAGGAAGAGAGA 336
 QY 301 atgagacagaagctatccagagctgtgagacagactcgaagagagagagagagat 360
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 Db 337 ATGACAGAAAGCTATCCAGAGCTGTAGCCGATGACTGACGAGGCAAGAGAGAGAT 396
 QY 361 gaattgtagtccaaatcacaatgataataaagagagagagagagagagagagat 420
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 Db 397 GAATGTGATCCAGAGCTCAGATGATATTTGAGAGAGAGAGAGATGATGATCTCAC 456
 QY 421 aaccatacataaagaagaacaaatgaatgatttgaactatttgaactactagtaagg 480
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 Db 457 AACCCATATATAAAGAAAGACATGAATGATTTGATTAAGAAAGCTGTGATTAAGG 516
 QY 481 caatttggaaagattatttggttcgagagagagagagagagagagagagagagat 540
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 Db 517 CACTTTTGGGAAGTTATTTTGTGTTGCGAGAGAGCAAGTGAATAATCTACGCTATGAA 576
 QY 541 gattctgaagaagaagatcatatttgcacaaagatgaatgagacacacacttcaatgaag 600
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 Db 577 GATTCGAAAGAAAGATCATATATGCAAGATGAGAGGACGACATCTGACATGAGAG 636
 QY 601 cagagatataaagaacactagacatccctttaaactccttgaataatctcctccagac 660
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 Db 637 CAGAGTTTAAAGAACACACGACATCCATTCATTCATTCATTCATTCATTCATTCAT 696
 QY 661 aaaagacagttgttcttgatgagatgagatgagagagagagagagagagagagat 720
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 Db 697 AAAAGACCGTTGTGTTGTGATGAAATGTTAATGGGGAGAGCTGTTTTCATATT 756
 QY 721 gtcgagagagcgggtgtctctcagagagcgcacagttctcagatgagagagagat 780
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 Db 757 GTCGAGAGAGCGCGGTCTCTGAGAGACGACAGCTTCTATGATGAGAAATGTCTC 816
 QY 781 tgccttgagactatcactatcccgaaagaatgtgacgagatcctcaagtgtgagagatc 840
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 Db 817 TGCTTTGAGACATATCTACATTCGAAAGATTTGTAACGAGATCTCAAGTTGGAGAAATTT 876
 QY 841 aatgttgagacaaagtgccacataaaatcaagatttggacttgcagaagagagat 900
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 Db 937 CACAGATGACAGTACATGAGAGACATCTCTGTGATGACACAGATATCTGCGACAGAGAT 996
 QY 961 gtagaagaataatgactatgagcagagacagatgagagagagagagagagagagat 1020
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 Db 997 ATTAGAAGATATGATGATGAGCGGAGCTGTGAGAGCTGTGAGGCTGTGATGATGAT 1056
 QY 1021 tgaatgatgtgtgat 1080

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Db 1057 TGAATGATGTGGAGGTTGCTTCTTACAAACGAGATCATGAGAACTCTTGTACT 1116
1081 aatattatggaagacttaatttctctgaaacactctctcagatgcaaatcatgtct 1140
Db 1117 AATACCTATGGAAGACATCAAAATTCCTCCCAACCTCTCTTCAGATCCAAAGCATGCT 1176
1141 tcaaggtctctgataaagatccaataaacgctctggtggaagacagatgatgcaaa 1200
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Qy 1261 gcttgtaacctctttaaacctcaagtaaacatctgagacagatcagatatttgatga 1320
Db 1297 GCTTGATCTCTCTTTTAAGCTCAAGTACATCTGAGACACCAAGATATTCGATGA 1356
Qy 1321 agaattacagctcagactataccaatacacaccacccaataaatat 1366
Db 1357 AGAATTACAGCTCAGCTATTTACAAATACACCACTGAAAGTGT 1402
RESULT 11
AF039943 2277 bp mRNA VRT 04-JAN-1998
LOCUS Gallus gallus serine/threonine protein kinase (akt1) mRNA, complete
DEFINITION cds
ACCESSION AF039943
VERSION AF039943.1 GI:2745888
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2277)
AUTHORS Theelen,M., Swinkels,S.U.M., de Jong,M.D.M., Thomas,A.A.M.,
Verkrel,A.J., Hanafusa,H. and Humbel,B.
TITLE The differential expression of Akt during the cell cycle is
regulated at the translational level
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2277)
AUTHORS Theelen,M., Kornbluth,S. and Hanafusa,H.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-1997) Mol. Cell Biology, Utrecht University,
Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES
source
1..2277
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gene 1..2277
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466..1908
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FGKVLVKEKATGRYAYAMILKKEVIVADEVAHTTERRVLONSHHPFLVALKYSFO
THDRLCFVMEVANGELFPHLSREYFESDRARFEGALIVSALDYLSKNNVYDRIK
LENIMLDKNGHKITIDFGCKKCGIKDGNMTKPCGPEYLAPEVLEDNDYGAQVWG
LGVNTEKMGCRUPTFNDHEKLFELILAEELRFPPTTISPEKSLSLGKLDKDPQRL
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BASE COUNT
ORIGIN

672 a 490 c 549 g 566 t

Query Match 55.0%; Score 850.6; DB 5; Length 2277;
Best Local Similarity 76.0%; Pred. No. 1,1e-185;
Matches 1106; Conservative 0; Mismatches 334; Indels 15; Gaps 4;
Qy 5 gtcacatgagcagtgatcaccatgtgaaagagtggttgcagaagagagagatat 64
Db 460 GCCATTATGATTAAGTACGATGAGTAAGGAAGATGCGTCCCAACGAGGAGATAT 519
Qy 65 ataaaaacgagggccagatactctcttgaagacagatggtccatcattagatat 124
Db 520 ATCAAAAACATGAGGCCACGCTATTTTAAACAATGAGCACATTTTATGCTGTAC 579
Qy 125 aagaagaacctcaagatggtgattac---ctatccctcacaaccttctagtgga 181
Db 580 AAGGACGACCGGCAAGACGTTGACCAACGAGATTCACCTTTAATATACCTTCAGTAGCT 639
Qy 182 aaatgcagtttaagaaacagacagcaaacgcaaacattataatcagatgctc 241
Db 640 CAGTGCAGCTGATGAAGACAGAACGACCTAAACCAACATTTATCATATGCTCCTC 699
Qy 242 cagtgactactgtatagagagaacattcattgatatcactcagaagagagagataa 301
Db 700 CAGTGGACACAGTAATTTGAAGAACATTTTCATGTGAGACTCCAGAGAGCGGGAAGAA 759
Qy 302 tggacagaagctatccaggtctgtagcagacagactgcaagagcaagaagagagatg 361
Db 760 TGGACAAAAGCTATCCAACTGTTCGACAGCGCTCAAGAACGAGAGAGAGATGATG 819
Qy 362 aattgagtcacactcacaatgataatagagagagagatgagatgctctaca 421
Db 820 GATTTTGAATCTGTTCTCTCTCTAGTAAATTCAGGTGCTGAAGAAATGGAAGCTTCTAG 879
Qy 422 accatcataaa---agaaagacaaatgagatgttgcactattgaaactcaggttaa 478
Db 880 ACAAGCCAAACACAAAGTACCATGATGATTTGAATTCCTTTAAGCTACTGGGAAAA 939
Qy 479 ggcactttgggaaagtatttctgctcagaaagagcaagtgaaataactatgctatg 538
Db 940 GGCACCTTTTGAAGAGCATTTTATGTTAAAGAAAACGACGAGATTTATGCTTAG 999
Qy 539 aagaattcagaagaagaatcattatcgaagaatgaaagtggcacactcaactgaa 598
Db 1000 AAAATCTGTAAGAGAGAGTATTGTAGCAAGAGAAAGATACACACGCTGACAGAA 1059
Qy 599 agagaatataaagaacacatagacatcccttttaacactccttgaatactccctcag 658
Db 1060 AACCGCTTTTACAGAACTCAGCGCATTCATTTTAACAGCTTTAAAGTATTCCTTCAAG 1119
Qy 659 acaaaagaccgtttgttcttgatgaaatagttaatgagggcgagctgttctcat 718
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Qy 719 ttgtcagagagaggtgttctctcagagccgacacgtttctatgtgcagaatgtgc 778
Db 1180 CTGTGAGAGAGCGGTGATTTTCTGAAAGACGGCGCGTGTATATGGCTGAGATTTGT 1239
Qy 779 tctgccttgagcatctacatctccgaaaga---tctgtaccgctatcacaagtggag 835
Db 1240 TCAGCGCTGATTTACTCGATTCAGAGAAAGATGCTGTGACAGAAATTTGAAGCTGGA 1299
Qy 836 aatcattatgctgacaagaatgagccacataaaatactacagatttggacttgcagaaga 895
Db 1300 AATCTTATGCTGATTAAGACGCGGACATTAATAATTAACAGCTTTGAGATATTAAGAA 1359
Qy 896 ggaatacagatgacagccacatgaaagacattctgtggaactcccaataatctggacaa 955
Db 1360 GGCATTAAGATGACCAACCAATGAAGACTTCTGTGGCACTCAAGATATCTTGACCA 1419
Qy 956 gaagtttgaagaataatactatgagccagagtagactggtggggccttagaggtcttc 1015
Db 1420 GAGGTCTGAGAGATTAATGACTATGTGCTGCGAGTGGACTGAGGAGATTTAGAGATTG 1479
Qy 1016 atgatgaaatgactgtgtgaggttactcttctacacaggaacatgagaacttct 1075

Db	1480	ATGATGAATGATGATGTGGCCGGCTCCCTTTTACAAATCAGGACCATTGAAAGCTCTTT	1539
Qy	1076	gaatlaataatgaatgaagacatlaattccctcgacacictcttcagatgcaaaatca	11335
Db	1540	GAATCATTCCTTATGAGAAAGATTAGATTTCACGCGACTTGTGCACCTGAACAAATCT	15998
Qy	1136	ttgccttcagggcgtctgtataaaggatccaataaagcgcttggtaggagaccagatg	1195
Db	1600	CTCTTGTCAGGTTTGGTGAGAAAGATCCCTAAACCAAGTTTAGGAGCGCTCTGATAT	1659
Qy	1196	gcaaaagaattatgagaccgagttcctctctcgagtaactgycgaagatgtatagat	12558
Db	1660	GCCAGGAGATTATGACGACCAAAATCTTGTGCGATTGTTGGCAAGATGTATACGGG	1719
Qy	1256	aaaaagcttbaactcctttaaacttaagtaaacctcgagacagatatactgataattt	1315
Db	1720	AAGAGCTTGACTCCATTTTAAGCCACAAGTTTACATCTGAAACAGATACAAGATATCTT	1779
Qy	1316	gataagaatttaacagcttcagactatacaataaacccactgaaataatgataagat	13757
Db	1780	GATAAACAATTTTACAGCAGCAGATGATTACATATCTCTCTCGACCAC-----GATGAC	18333
Qy	1376	ggtatgacatcgatgagcaatgagagcgagcgacatcttcctcaaatllctactactg	14335
Db	1834	AGCATGGATTGTGTAGACATGTAGAGAAAGACCTCATTTTCTCAGTTCCTATTCAGCC	18998
Qy	1436	agtgagcagaaata 1450	
Db	1894	AGTGAACCGCTTAA 1908	

RESULT	12
LOCUS	AF317656
DEFINITION	AF317656 Xenopus laevis Akt mRNA, complete cds.
ACCESSION	AF317656
VERSION	AF317656.1 GI:12539653
KEYWORDS	
SOURCE	African clawed frog.
ORGANISM	Xenopus laevis
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
AUTHORS	1 (bases 1 to 1808)
TITLE	Andersen,C.B., Sakaue,H., Roth,R.A. and Conti,M.
JOURNAL	The protein kinase B/Akt is required for resumption of meiosis in Xenopus oocytes
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 1808)
TITLE	Andersen,C.B. and Conti,M.
JOURNAL	Direct Submission
REFERENCE	Submitted (31-OCT-2000) Obstetrics and Gynecology, Stanford University, 300 Pasteur Dr., Stanford, CA 94305-5317, USA
FEATURES	Location/Qualifiers
SOURCE	1..1808
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	/dev_stage="oocyte"
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BASE COUNT	585 a	347 c	406 g	470 t
ORIGIN				

Query Match	51.0%;	Score 789.2;	DB 5;	Length 1808;
Best Local Similarity	73.8%;	Pred. No. 1.6e-171;		
Matches 1075; Conservative	0;	Mismatches 363;	Indels 18;	Gaps 5;

OY	11	atgagcgaatgttaccatttgyaaagaagtttgggtlccaagaagagggagataataa	70
Db	1	ATGAATGAAGTAGGATAGTAGTAAGGAAGGCTGCTGCACAAAGAGGTGAATCATTAAG	60
OY	71	aactgagagccaagaatacttccttltbgaagacagatggtccatltcaagataaag	130
Db	61	ACCTGGCCCTCCCTCTACTCTCTCTCAAAATCTACGGTACTTTTCATTTGGGTCAAAAG	120
OY	131	aaacctgaagatgag---attacatlaacccctcaagacactltcaagtgagcaaatgc	187
Db	121	CGTCCACAAAGATGTTTGACACAGTTTGGAAATCTCTTTAAATATTTCTGTAGCCAAATGT	180
OY	188	cagtaatgaaacaagaacagaccaaagccaacacatltlaatcagatgtctccagtg	247
Db	181	CAGGTAGTAGAGACAGAAAGACAAACCAATTTATTCATTTGGTGGTCTCCACGTGG	240
OY	248	actactgttataagagagaacatltcaltgtatatactccagaaggaagaagatgaga	307
Db	241	ACCACAGTAATTTGGAAGAACATTTTCATGTGTGATTTCTCAAGAGCGCGGAAGATGGATT	300
OY	308	gaagctatccagcgctgtgtacagacagactcagagaggaagaagaagaagaatgt	367
Db	301	CAGGTGATACAAACATGTATGCCACAACTCAAGAGCAGAGACAGAAATGATGGAGTT	360
OY	368	agttccaac---ttcacaatltgataataatagagaggaagatgtgaltgtcctcaaac	424
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OY	425	catcataa---agaagacacatgaatgtatgttgcactatltgaacctactagttaaagc	481
Db	421	AAACCAAAACATTAAGTTTACATTAATGAATTTAGTATCTCAAGCTTTTGGGGAAGA	480
OY	482	actlttggagaagtatlttggcttcgagagaaggaagaagtgtgaataactatgtcataag	541
Db	481	ACGTTTGGAAAAAGTTATTTTGTATTAAGAGAGAAAGCAACGACAGATTTTACGTTATGAA	540
OY	542	attctgaaagaagaagtcattatltgtcaagaagatltgaatgtgcacacactcaactgaagc	601
Db	541	ATTTTAAAAAAGAAAGTATTGTGTGCAAAAGATCACTACCCACACGTTACGGAAG	600
OY	602	agaagtataaagaacactagacatccctlttacaatcctltgaataatacttcctcagaca	661
Db	601	CGCGCTCCACAGAAATTTGAGCAATCCCTCTTAACACATTAATAATTTCTTTCAGAC	660
OY	662	aaagacgtttgtgttltgtatgaatgaatgaatgtgagggagagcgtgttccatltg	721
Db	661	CATGATCCCTTATGTGTTTGTGATGTAGATATGCCAATGAGAGAGATTATTTCTCCACTTA	720
OY	722	tcgagagagcgagtgctctcctgagagccgcacacagttcctcaltgtgtcgaaatgtctct	781
Db	721	TCAAGAGAACTATATTCTGTGAAGATCGTGCCGGTTTATGTGGGGCAGAGATTGTTCTG	780
OY	782	gaccttgaactatctacatltcgg---gaaagatgtgtgaacgtgtatctccaagtttgaag	838
Db	781	GCTTTAGTATTTCTTCATTTCTGAGAAAAAATGTATTTTACAGAGACCTTGAAGTTGGA	840
OY	839	ctaattctgtgacaagaatgtgcccacataaaatcacaagatlttgactgtcaagaaggg	898
Db	841	CTAATGCGTGGACAAAGACGAGCNCATTAAGATTAACATTTTGTGACGTGTGCAAAAGGA	900
OY	899	atcacaagatcagccacacatgaagaactctgtgtgcaatccagaaataatctgacacag	958
Db	901	ATTAAGAATGTGAAGCACACATGATGAACCTTCTGTGGAACACCAAAATATCTGCTCTGAG	960

QY	839	ctaagctgcygaaanaagatgagccacataaataatcacagattttggaactttgcaagaagagg	898
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QY	899	atcacagagctgcagccaccatgaagacattctctgcaaccgaatctgtgcacagag	958
Db	2070	atcaagagatggcgccactatgaaacatttttgcgaagaccggaggaactgtgccccctgtg	2129
QY	959	gttgtaagaagaataatgacatctatgcccagacagtagaactgtgtggagcctaaagtctcatg	1018
Db	2130	gtgctggaagacaagacactacgcccgtcagcagtgacagactgtgggggctggcctggctcag	2189
QY	1019	tatgaataatgatgtgtggaaggttaccttctctacaacccagacatgagaacattttgaa	1078
Db	2190	tatgagatgatgtgtggccgctgtgccccttctcacaaccagacagagaaactgtttcgag	2249
QY	1079	ttaataatgaagaaagacattaaatttctctgaaacactctcttcagatgacaaatcatgt	1138
Db	2250	ctgattctctatgagagaaatccgcttcccgccacactcgcgcctgagagcccaagctccctg	2309
QY	1139	ctttcagaggtctgtataaagatccacaataaagccgtgtgtggaagacagatgatga	1198
Db	2310	ctcttcgggggctcctcaagaagagacccttcacagagagcttggtgggggctcttagaatgcc	2369
QY	1199	aagaagaattatgagacacagttctctctctgtgagtaaatctggaagatgatataaa	1258
Db	2370	aagcagatcatgacacacccggttttgcacacatctgctgagagatgtatgagaaag	2429
QY	1259	aagctgtacctctctttaaaccctaaagtaaatcttggaagacatcagataatttgat	1318
Db	2430	aagctgagacccacacttttaagccccaaggtcactcttgagacacagagatatttcgat	2489
QY	1319	gaagaaattcacagctcacactcttacaataacaccacgtgaanaaatatgatgagatgt	1378
Db	2490	gagagattcacacagctcaatgatactacacactacgcccgtg-----atcacagatcacac	2543
QY	1379	atgagctgcatgagacaatgagagagcgccgcacattccctcacaatttctctactctgcaat	1438
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QY	1439	ggagagagataaagtc 1453	
Db	2604	ggcacagccctgagcg 2618	
RESULT 14			
MMSTPK	LOCUS	2626 bp	mRNA
DEFINITION	M.musculus mRNA for serine-threonine protein kinase.	11-MAR-1993	
ACCESSION	X65687		
VERSION	X65687.1	GI:287806	
KEYWORDS	protein kinase; serine/threonine protein kinase.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 2626)		
REFERENCE	2 (bases 1 to 2626)		
REFERENCE	Bellacosa, A., Franke, T.F., Gonzalez-Portal, M.E., Datta, K., Taguchi, T., Gardner, J., Cheng, J.O., Testa, J.R. and Tschlis, P.N.		
TITLE	Structure, expression and chromosomal mapping of c-akt: relationship to v-akt and its implications		
JOURNAL	Oncogene 8 (3), 745-754 (1993)		
MEDLINE	93173519		
FEATURES	Location/Qualifiers		
SOURCE	1..2626		
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Query Match	Best Local Similarity	Matches 1044:	Conservative	0;	Mismatches	396;	Indels	15;	Gaps	4;
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Db	281	ACCATGAACGAGATGACATTTGTGGAAGGAGGGCTGGCTGCACCAACGAGGGGAATATATTT	340							
QY	68	aaaacttgagagccagaatacttccttlttgagaagagaatggtccatcatagaataaa	127							
Db	341	AAAACCTGGCGGCCACGCTACTTCTCCTCAAGAACGATGGCCACTTATTTGGCTACAG	400							
QY	128	gagaaacctcaagatltgagat---ttacctatcccccaaaccttltcagltgycaaa	184							
Db	401	GAACGGCTTCAGGATGTGGATCAGGAGAGATGCCACACTCAACACTTCTCAGTGGACAA	460							
QY	185	tggcagttatagaagaacgaagacgaagccaaagccaaacattataatcagatgtctcag	244							
Db	461	TGCCATCGATGAACACGAGACGGGCAAGGGCCCAACCTTATATCTCGCTGCTCGC	520							
QY	245	tggactactgttatagaagaacattcatgtatagatactccagagaggaagaagaatgg	304							
Db	521	TGGACCAAGTCATTGACGCGACCTTCCATGTGGAAACGCTTGAGGAGCGGGAAGATGG	580							
QY	305	acagaagctatccagctgttagcagacagacactgacagagcaagaagaagaagaatgat	364							
Db	581	GCCACCGCCATTGACAGCTGTGGCCGATGACTCAAGAGCGCAGAAAGACAGCATGGAC	640							
QY	365	tgtatgccaaacttacaacaattgataataatagagagaagaagaatgtagtgcctacaac	424							
Db	641	TTCCGATCAGGCTCCACCGATGACAAACACAGGGGGCTGAAAGATGAGAGTGTCCTGGCC	700							
QY	425	catc---ataaagaagaacaatgaatgatttgaactattggaactactagtgaaagc	481							
Db	701	AAGCCCAAGCACCGTGTACCATGACAGATTGAGTACCTGAAACTACTGCGAAGGCC	760							
QY	482	acttlttggaagatatttltgttcgagagaaggaaggtggaataataactatgtcatgaag	541							
Db	761	ACCTTTTGGGAAAGTATCTGTGTGTAAGAGAGAGCCACAGGCCCGCTACTATGCGCATGAG	820							
QY	542	atttcgaagaagaagatcatatatgtgcaagaagatgaagtgtgacacacactcctaactgaagc	601							
Db	821	ATCCCTCAAGAGGAGTGTATCGTCGCCAAGAGATAGGTTGGCCACAGCTTACGGAAC	880							
QY	602	agagatttaagaagaacatagacatoccccttlttaacatcccttggaataatcccttcagaca	661							
Db	881	CGTGTCTGCGAAGACTCTAGGCAATCCCTTCTTACGGGCCCTCAAGTACTATTTCCAGACC	940							
QY	662	aaagacglttltgttlttltgaltgaatatgtltaatgggggagagctgttlttccattg	721							

Db 941 CACGACGGCTCTGCTTTGTGATGATGATGCCAAGGGGGGAGCTCTTTCACACTG 1000
QY 722 tcgagagagcgggtgtctctctgagagccgacacgttctatgtgcagaattgtctct 781
Db 1001 TCTCGAGACGGCGTGTCTTCCGAGGACCGGCCCCGCTTCTATGTGTCGGAGATGTGTCT 1060
QY 782 gaccttgcattctacattccgynaaga--ttgttaccgttgatctcaagtgtgaaat 838
Db 1061 GCCCTGACTACTTGCACTCCGAGAGAACGTGTGTACCGGAGACTGAAGCTGGAGAAC 1120
QY 839 ctaatgtctgacaagaatgtccacataaaatatacagatttggactttgcaagaagg 898
Db 1121 CTCATCTGGACAGGACGGGACATCAATTAACGGACTCGGCTGTGACGAGAGGG 1180
QY 899 atcacagatgcagccacccatgaagacattctgtgacccccaatctgtgaccagag 958
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Db 1241 GTGCTGAGAGACAAAGACTACGGCCGTGAGTGAAGTGTGGGGGCTGGGCGTGTATG 1300
QY 1019 tatgaatagtgtgtgagaggttaccttctacaaccagagacatgagaacttttga 1078
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QY 1139 ctttcagagctctgtgataaagatcccaataaagcctgtgtgagagacagatgtga 1198
Db 1421 CTCTCGGGCTGCTCAAGAGAGACCTTACACAGAGCTCGGTGGGGGCTGTGAGATGCC 1480
QY 1199 aaagaataatgagacacagtttctctctgtgagtaactgtgcaagaatgtataaa 1258
Db 1481 AAGGATATGATGACAGCAGCGGTCTTGTGCCAATGCTGTGGAGATGTGTATGGAAG 1540
QY 1259 aagctgttaccctctttaaactcaagtaacatctgagacagatactgatatgtgat 1318
Db 1541 AAGCTGAGGCCACCTTTCAAGCCCGAGGTCACTCTGAGACTGACCCAGGATTTTCGAT 1600
QY 1319 gaagaattacagctcagaactatatacaaacacacactgtgaaatataatgtatgt 1378
Db 1601 GAGGACTTCAAGCTCAGATGATACACATCACGCCGCTG-----ATCAAGATGACAG 1654
QY 1379 atggaactgcatgagacatgagagggcgccgcatctccccaatttctcactctgaat 1438
Db 1655 ATGGAATGTGTGACAGTGAAGGGAGCGGCACTTCCGAGTTCCTTACAGCCAGT 1714
QY 1439 ggaagagataatgtc 1453
Db 1715 GGCACAGCCTGAGGC 1729

RESULT 15
MUSRAC 1513 bp mRNA ROD 24-MAY-1994
LOCUS MUS musculus protein kinase mRNA, complete cds.
DEFINITION M94335
ACCESSION M94335 GI:200641
VERSION M94335.1
KEYWORDS protein kinase.
SOURCE Mus musculus CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1513)
AUTHORS Bousquets,X. and Powell,C.T.
TITLE Complete nucleotide coding sequence for murine rac (related to A
and C kinases) protein kinase
JOURNAL Unpublished
FEATURES
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